(www-ncbi.nlm.nih.gov/Web/Genebank/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (www-ebi.ac.uk/ebi_docs/embl_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequence queries (BLASTN, BLASTX and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, *12*:76-80 (1994); Birren, *et al. Genome Analysis, 1*: 543-559 (1997)).

A1 cont

Please delete the paragraph at page 22, lines 5 to 11, and replace it with the following paragraph:

A2

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (available on the World Wide Web at genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (available on the World Wide Web at genome.wi.mit.edu/cgi-bin/www-STS_Pipleine) or GeneUp (Pesole *et al., BioTechniques 25*:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.

In the Claims:

Please cancel non-elected claims 2-9, without prejudice to or disclaimer of the subject matter contained therein.

Please amend the claims as follows: